

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/574,045
Source: JFWP
Date Processed by STIC: 04/07/2006

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/574,045

DATE: 04/07/2006

TIME: 11:02:40

Input Set : A:\14875-157US1.txt

Output Set: N:\CRF4\04072006\J574045.raw

3 <110> APPLICANT: Matsushima, Kouji
 4 Hashimoto, Shinichi
 5 Tsuchiya, Masayuki
 6 Hirata, Yuichi
 7 Yoshida, Kenji
 8 Ojima, Kazuyuki
 10 <120> TITLE OF INVENTION: PROTEIN EXPRESSED IN NK CELL
 12 <130> FILE REFERENCE: 14875-157US1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/574,045
 C--> 14 <141> CURRENT FILING DATE: 2005-03-28
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/14207
 15 <151> PRIOR FILING DATE: 2004-09-29
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-338331
 18 <151> PRIOR FILING DATE: 2003-09-29
 20 <160> NUMBER OF SEQ ID NOS: 53
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1473
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (87)..(1376)
 34 <400> SEQUENCE: 1
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 37 agagaacgtt agagggaaaat atatga atg ttg cca tct tta gtt ccc tgt gtt 113
 38 Met Leu Pro Ser Leu Val Pro Cys Val
 39 1 5
 41 ggg aaa act gtc tgg ctg tac ctc caa gcc tgg cca aac cct gtg ttt 161
 42 Gly Lys Thr Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe
 43 10 15 20 25
 45 gaa gga gat gcc ctg act ctg cga tgt cag gga tgg aag aat aca cca 209
 46 Glu Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro
 47 30 35 40
 49 ctg tct cag gtg aag ttc tac aga gat gga aaa ttc ctt cat ttc tct 257
 50 Leu Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser
 51 45 50 55
 53 aag gaa aac cag act ctg tcc atg gga gca gca aca gtg cag agc cgt 305
 54 Lys Glu Asn Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg
 55 60 65 70
 57 ggc cag tac agc tgc tct ggg cag gtg atg tat att cca cag aca ttc 353
 58 Gly Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe
 59 75 80 85

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61	aca caa act tca gag act gcc atg gtt caa gtc caa gag ctg ttt cca	401
62	Thr Gln Thr Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro	
63	90 95 100 105	
65	cct cct gtg ctg agt gcc atc ccc tct cct gag ccc cga gag ggt agc	449
66	Pro Pro Val Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser	
67	110 115 120	
69	ctg gtg acc ctg aga tgt cag aca aag ctg cac ccc ctg agg tca gcc	497
70	Leu Val Thr Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala	
71	125 130 135	
73	ttg agg ctc ctt ttc tcc cac aag gac ggc cac acc ttg cag gac	545
74	Leu Arg Leu Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp	
75	140 145 150	
77	agg ggc cct cac cca gaa ctc tgc atc ccg gga gcc aag gag gga gac	593
78	Arg Gly Pro His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp	
79	155 160 165	
81	tct ggg ctt tac tgg tgt gag gtg gcc cct gag ggt ggc cag gtc cag	641
82	Ser Gly Leu Tyr Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln	
83	170 175 180 185	
85	aag cag aca ccc cag ctg gag gtc aga gtc cag gct cct gta tcc cgt	689
86	Lys Gln Ser Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg	
87	190 195 200	
89	cct gtg ctc act ctg cac cac ggg cct gct gac cct gct gtg ggg gac	737
90	Pro Val Leu Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp	
91	205 210 215	
93	atg gtg cag ctc ctc tgt gag gca cag agg ggc tcc cct ccg atc ctg	785
94	Met Val Gln Leu Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu	
95	220 225 230	
97	tat tcc ttc tac ctt gat gag aag att gtg ggg aac cac tca gct ccc	833
98	Tyr Ser Phe Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro	
99	235 240 245	
101	tgt ggt gga acc acc tcc ctc ttc cca gtg aag tca gaa cag gat	881
102	Cys Gly Gly Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp	
103	250 255 260 265	
105	gct ggg aac tac tcc tgc gag gct gag aac agt gtc tcc aga gag agg	929
106	Ala Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg	
107	270 275 280	
109	agt gag ccc aag aag ctg tct ctg aag ggt tct caa gtc ttg ttc act	977
110	Ser Glu Pro Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr	
111	285 290 295	
113	ccc gcc agc aac tgg ctg gtt cct tgg ctt cct gcg agc ctg ctt ggc	1025
114	Pro Ala Ser Asn Trp Leu Val Pro Trp Leu Pro Ala Ser Leu Leu Gly	
115	300 305 310	
117	ctg atg gtt att gct gct gca ctt ctg gtt tat gtg aga tcc tgg aga	1073
118	Leu Met Val Ile Ala Ala Leu Leu Val Tyr Val Arg Ser Trp Arg	
119	315 320 325	
121	aaa gct ggg ccc ctt cca tcc cag ata cca ccc aca gct cca ggt gga	1121
122	Lys Ala Gly Pro Leu Pro Ser Gln Ile Pro Pro Thr Ala Pro Gly Gly	
123	330 335 340 345	
125	gag cag tgc cca cta tat gcc aac gtg cat cac cag aaa ggg aaa gat	1169

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126	Glu	Gln	Cys	Pro	Leu	Tyr	Ala	Asn	Val	His	His	Gln	Lys	Gly	Lys	Asp
127					350					355						360
129	gaa	ggt	gtt	gtc	tac	tct	gtg	cat	aga	acc	tca	aag	agg	agt	gaa	1217
130	Glu	Gly	Val	Val	Tyr	Ser	Val	Val	His	Arg	Thr	Ser	Lys	Arg	Ser	Glu
131					365				370						375	
133	gcc	agg	tct	gct	gag	ttc	acc	gtg	ggg	aga	aag	gac	agt	tct	atc	atc
134	Ala	Arg	Ser	Ala	Glu	Phe	Thr	Val	Gly	Arg	Lys	Asp	Ser	Ser	Ile	Ile
135					380				385						390	
137	tgt	gcg	gag	gtg	aga	tgc	ctg	cag	ccc	agt	gag	gtt	tca	tcc	acg	gag
138	Cys	Ala	Glu	Val	Arg	Cys	Leu	Gln	Pro	Ser	Glu	Val	Ser	Ser	Thr	Glu
139					395				400						405	
141	gtg	aat	atg	aga	agc	agg	act	ctc	caa	gaa	ccc	ctt	agc	gac	tgt	gag
142	Val	Asn	Met	Arg	Ser	Arg	Thr	Leu	Gln	Glu	Pro	Leu	Ser	Asp	Cys	Glu
143					410				415						425	
145	gag	gtt	ctc	tgc	tag	tgtatgggttt	ctccttatcaa	cacacgcccc	cccccc	1416						
146	Glu	Val	Leu	Cys												
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159	1				5				10							15
161	Leu	Gln	Ala	Trp	Pro	Asn	Pro	Val	Phe	Glu	Gly	Asp	Ala	Leu	Thr	Leu
162					20				25							30
164	Arg	Cys	Gln	Gly	Trp	Lys	Asn	Thr	Pro	Leu	Ser	Gln	Val	Lys	Phe	Tyr
165					35				40							45
167	Arg	Asp	Gly	Lys	Phe	Leu	His	Phe	Ser	Lys	Glu	Asn	Gln	Thr	Leu	Ser
168					50				55							60
170	Met	Gly	Ala	Ala	Thr	Val	Gln	Ser	Arg	Gly	Gln	Tyr	Ser	Cys	Ser	Gly
171					65				70							80
173	Gln	Val	Met	Tyr	Ile	Pro	Gln	Thr	Phe	Thr	Gln	Thr	Ser	Glu	Thr	Ala
174					85				90							95
176	Met	Val	Gln	Val	Gln	Glu	Leu	Phe	Pro	Pro	Pro	Val	Leu	Ser	Ala	Ile
177					100				105							110
179	Pro	Ser	Pro	Glu	Pro	Arg	Glu	Gly	Ser	Leu	Val	Thr	Leu	Arg	Cys	Gln
180					115				120							125
183	Thr	Lys	Leu	His	Pro	Leu	Arg	Ser	Ala	Leu	Arg	Leu	Leu	Phe	Ser	Phe
184					130				135							140
186	His	Lys	Asp	Gly	His	Thr	Leu	Gln	Asp	Arg	Gly	Pro	His	Pro	Glu	Leu
187					145				150							160
189	Cys	Ile	Pro	Gly	Ala	Lys	Glu	Gly	Asp	Ser	Gly	Leu	Tyr	Trp	Cys	Glu
190					165				170							175
192	Val	Ala	Pro	Glu	Gly	Gly	Gln	Val	Gln	Lys	Gln	Ser	Pro	Gln	Leu	Glu
193					180				185							190
195	Val	Arg	Val	Gln	Ala	Pro	Val	Ser	Arg	Pro	Val	Leu	Thr	Leu	His	His
196					195				200							205
198	Gly	Pro	Ala	Asp	Pro	Ala	Val	Gly	Asp	Met	Val	Gln	Leu	Leu	Cys	Glu

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199	210	215	220	
201	Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu			
202	225	230	235	240
204	Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu			
205	245	250	255	
207	Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu			
208	260	265	270	
210	Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser			
211	275	280	285	
213	Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val			
214	290	295	300	
216	Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala			
217	305	310	315	320
219	Leu Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser			
220	325	330	335	
222	Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala			
223	340	345	350	
225	Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val			
226	355	360	365	
228	Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr			
229	370	375	380	
231	Val Gly Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu			
232	385	390	395	400
234	Gln Pro Ser Glu Val Ser Ser Thr Glu Val Val Asn Met Arg Ser Arg Thr			
235	405	410	415	
237	Leu Gln Glu Pro Leu Ser Asp Cys Glu Glu Val Leu Cys			
238	420	425		
241	<210> SEQ ID NO: 3			
242	<211> LENGTH: 2005			
243	<212> TYPE: DNA			
244	<213> ORGANISM: Homo sapiens			
246	<220> FEATURE:			
247	<221> NAME/KEY: CDS			
248	<222> LOCATION: (88)..(1410)			
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254	aagagaacga tagagaaaa tatatga atg ttg cca tct tta ggc ccc atg ctg		114	
255	Met Leu Pro Ser Leu Gly Pro Met Leu			
256	1	5		
258	ctc tgg acg gct gtg ctg ctc ttt gtt ccc tgt gtt ggg aaa act gtc		162	
259	Leu Trp Thr Ala Val Leu Leu Phe Val Pro Cys Val Gly Lys Thr Val			
260	10	15	20	25
262	tgg ctg tac ctc caa gcc tgg cca aac cct gtg ttt gaa gga gat gcc		210	
263	Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp Ala			
264	30	35	40	
266	ctg act ctg cga tgt cag gga tgg aag aat aca cca ctg tct cag gtg		258	
267	Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln Val			
268	45	50	55	
270	aag ttc tac aga gat gga aaa ttc ctt cat ttc tct aag gaa aac cag		306	

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271	Lys	Phe	Tyr	Arg	Asp	Gly	Lys	Phe	Leu	His	Phe	Ser	Lys	Glu	Asn	Gln	
272		60					65						70				
274	act	ctg	tcc	atg	gga	gca	gca	aca	gtg	cag	agc	cgt	ggc	cag	tac	agc	354
275	Thr	Leu	Ser	Met	Gly	Ala	Ala	Thr	Val	Gln	Ser	Arg	Gly	Gln	Tyr	Ser	
276		75						80				85					
278	tgc	tct	ggg	cag	gtg	atg	tat	att	cca	cag	aca	ttc	aca	caa	act	tca	402
279	Cys	Ser	Gly	Gln	Val	Met	Tyr	Ile	Pro	Gln	Thr	Phe	Thr	Gln	Thr	Ser	
280		90						95			100			105			
282	gag	act	gcc	atg	gtt	caa	gtc	caa	gag	ctg	ttt	cca	cct	cct	gtg	ctg	450
283	Glu	Thr	Ala	Met	Val	Gln	Val	Gln	Glu	Leu	Phe	Pro	Pro	Pro	Val	Leu	
284								110			115			120			
286	agt	gcc	atc	ccc	tct	cct	gag	ccc	cga	gag	ggt	agc	ctg	gtg	acc	ctg	498
287	Ser	Ala	Ile	Pro	Ser	Pro	Glu	Pro	Arg	Gly	Ser	Leu	Val	Thr	Leu		
288								125			130			135			
290	aga	tgt	cag	aca	aag	ctg	cac	ccc	ctg	agg	tca	gcc	ttg	agg	ctc	ctt	546
291	Arg	Cys	Gln	Thr	Lys	Leu	His	Pro	Leu	Arg	Ser	Ala	Leu	Arg	Leu	Leu	
292								140			145			150			
294	ttc	tcc	ttc	cac	aag	gac	ggc	cac	acc	ttg	cag	gac	agg	ggc	cct	cac	594
295	Phe	Ser	Phe	His	Lys	Asp	Gly	His	Thr	Leu	Gln	Asp	Arg	Gly	Pro	His	
296								155			160			165			
298	cca	gaa	ctc	tgc	atc	ccg	gga	gcc	aag	gag	gga	gac	tct	ggg	ctt	tac	642
299	Pro	Glu	Leu	Cys	Ile	Pro	Gly	Ala	Lys	Glu	Gly	Asp	Ser	Gly	Leu	Tyr	
300		170						175			180			185			
302	tgg	tgt	gag	gtg	gcc	cct	gag	ggg	ggc	cag	gtc	cag	aag	cag	agc	ccc	690
303	Trp	Cys	Glu	Val	Ala	Pro	Glu	Gly	Gly	Gln	Val	Gln	Lys	Gln	Ser	Pro	
304								190			195			200			
306	cag	ctg	gag	gtc	aga	gtg	cag	gct	cct	gta	tcc	cgt	cct	gtg	ctc	act	738
307	Gln	Leu	Glu	Val	Arg	Val	Gln	Ala	Pro	Val	Ser	Arg	Pro	Val	Leu	Thr	
308								205			210			215			
310	ctg	cac	cac	ggg	cct	gct	gac	ccc	gct	gtg	ggg	gac	atg	gtg	cag	ctc	786
311	Leu	His	His	Gly	Pro	Ala	Asp	Pro	Ala	Val	Gly	Asp	Met	Val	Gln	Leu	
312								220			225			230			
314	ctc	tgt	gag	gca	cag	agg	ggc	tcc	cct	ccg	atc	ctg	tat	tcc	ttc	tac	834
315	Leu	Cys	Glu	Ala	Gln	Arg	Gly	Ser	Pro	Pro	Ile	Leu	Tyr	Ser	Phe	Tyr	
316								235			240			245			
318	ctt	gat	gag	aag	att	gtg	ggg	aac	cac	tca	gct	ccc	tgt	ggg	gga	acc	882
319	Leu	Asp	Glu	Lys	Ile	Val	Gly	Asn	His	Ser	Ala	Pro	Cys	Gly	Gly	Thr	
320		250						255			260			265			
322	acc	tcc	ctc	ctc	tcc	cca	gtg	aag	tca	gaa	cag	gat	gct	ggg	aac	tac	930
323	Thr	Ser	Leu	Leu	Phe	Pro	Val	Lys	Ser	Glu	Gln	Asp	Ala	Gly	Asn	Tyr	
324								270			275			280			
326	tcc	tgc	gag	gct	gag	aac	agt	gtc	tcc	aga	gag	agg	agt	gag	ccc	aag	978
327	Ser	Cys	Glu	Ala	Glu	Asn	Ser	Val	Ser	Arg	Glu	Arg	Ser	Glu	Pro	Lys	
328								285			290			295			
330	aag	ctg	tct	ctg	aag	ggt	tct	caa	gtc	ttg	ttc	act	ccc	gcc	agc	aac	1026
331	Lys	Leu	Ser	Leu	Lys	Gly	Ser	Gln	Val	Leu	Phe	Thr	Pro	Ala	Ser	Asn	
332								300			305			310			
334	tgg	ctg	gtt	cct	tgg	ctt	cct	gcg	agc	ctg	ctt	ggc	ctg	atg	gtt	att	1074
335	Trp	Leu	Val	Pro	Trp	Leu	Pro	Ala	Ser	Leu	Leu	Gly	Leu	Met	Val	Ile	

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31
Seq#:32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date